SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HARADA, SHUN-ICHI
SAMPATH, K. T.
RODAN, GIDEON A.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING MORPHOGEN ANALOGS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
(B) STREET: 45 SOUTH STREET
(C) CITY: HOPKINTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 01748

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: VITO, CHRISTINE C.
(B) REGISTRATION NUMBER: 39,061
(C) REFERENCE/DOCKET NUMBER: CRP-126

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617)-248-7000
(B) TELEFAX: (617)-248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..1067
(D) OTHER INFORMATION: /product= "MOUSE TYPE 10 COLLAGEN PROMOTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGATCCTAA AACACTTAAG GATATTTCTG TAAGGCTGTG AAAGAGAAAA CCAACTACTT 60

ACACGGATGG AGACCATGTT TATTTCTTTG GGAGAAAAGC CTAATTGGGA CGCTTCGAGA 120

TCCCTATAGG AAATTGCACC AGTAGTCAAC TGGATTTTTA AAAGGCAAAG CTTGAGGATT 180

TTTTTTTCCC TTTGAAATGA ATGTAGCAAA CTTATGTAAG CACGGAATAG GATTATTAGT 240

TAACAGTCTT TTCAATTATA TGGGAAAATG AAAACTAGGG GAGCGTCTAA GGCCACTTGC 300

TGACCTTTGT GCAGCTGTTA AGTAAAGAAA GTAAACCCTC CAGGGATACT GAACAGCCAA 360

CTGTCATAAG TCCAGGGTGT CTTGCACTTG CTGTGACAAG TTTAAAATAT TTAATATGAC 420

TATACCTGAA ATATTTAATG CTATCTTTTT CATGCACCAG CTTCTAAGAG CTTTCCCTAA 480

AATCCTGATA TGCAAAAGAA TATACCAATA TTTTCCCCCT TGCCCCTGGC GCTTGTCTCC 540

CAAGTTAGCA AACACTTAGG TAAGCGATTT TTACAGAACT TTTTTCCCTA ATAACTGAAG 600

GACTAACATG ATGATTTAGA TCTATATTCT CCCCAAAAGG CGTCTCATAT TTTTGTATAT 660

TACCAAATAT TTTCAGTCAA ATAACACAAG AATGTATTTT AAAAATAAAA AGGGTGAATC 720

ATCATTCCAT CATGAACCAA CATTGGACTC AGAACTCCTA AAAGGAAAAC AGAAAAAAAA 780

AAAAAATCAT GCACAGCCGA AGCTATTAAT ATATAATGGA GACAAAGAGT TTATTTTTCA 840

ATGAGAATAA CAAGGAAAAA AGCCTGATTT TGTACGCCTG CCCGTTAGGA CTTCCCACCA 900

TAATTAGTGC TTCTTGCCCC TGAGAGGAGG AGCTTCGGCT CAGGGGAACT TCATGCAATA 960

AGGGAAGAAA ACAGTATAAA TACTCCAGGG CAGCCGTGGG GAAGGCATTA TCCACTGCTC 1020

CTGGGCAGAG GAAGCCAGGA AAGCTGCCCC ACGCATCTCC CAGCACC 1067

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "AP1 SEQUENCE A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGCTTGATGA CTCAGCCGGA A 21

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..10
(D) OTHER INFORMATION: /product= "AP1 SEQUENCE A MUTATION"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCTCATCA 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..25
(D) OTHER INFORMATION: /note= "Conserved domain of human c-fos"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Val Glu Gln Leu Ser Pro Glu Glu Glu Glu Lys Arg Arg Ile Arg
1 5 10 15

Arg Ile Arg Asn Lys Met Ala Ala Ala
20 25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /product= "AP-1 CONSENSUS SEQUENCE B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACTCAGC GCGGA 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /product= "MEF-2 CONSENSUS"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAAAAATAA C 11

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /product= "MEF-2 CONSENSUS MUTANT OLIGO"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAAACATAA A 11

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..11
(D) OTHER INFORMATION: /product= "MEF-2 MUTANT CONSENSUS"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAACATAA C 11